

1600

WB
Sector
Box 560



I hereby certify that this correspondence is being deposited with the US Postal Service with sufficient postage as First Class Mail in an envelope addressed to Box Sequence, Assistant Director for Patents, Washington, D.C. 20231 on the date shown below.

Date: March 20, 2001

By: Kay L. Ganglio

RECEIVED
MAR 20 2001
PATENT
Docket No. GC396-2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of)	
Brian S. Miller et al.)	Group Art Unit: 1652
Serial No.: 09/262,126)	Examiner: Rao, M
Filed: March 3, 1999)	
For: Modified Forms of Pullulanase)	

TRANSMITTAL LETTER FOR MISSING PARTS OF APPLICATION

BOX SEQUENCE
Assistant Director for Patents
Washington, D.C. 20231

Sir:

In complete response to the Notice to Comply with Requirements for Patent Applications containing Nucleotide Sequence and/or amino Acid Sequence disclosures dated February 27, 2001.

- ☒ Preliminary Amendment
- ☒ Statement of Sameness
- ☒ Paper copy of Sequence Listing (9 pages)
- ☒ Diskette copy of Sequence Listing
- ☒ Form PTO-1533 (copy of Notice to be returned with response); and

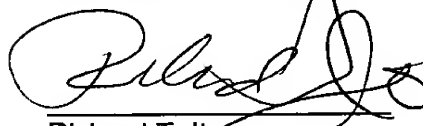
The Director is hereby authorized to charge any fees under 37 C.F.R. §§ 1.16, 1.17, and 1.21 that may be required by this paper, and to credit any

RECEIVED
MAR 29 2001
TECH CENTER 1600/2900

US Serial No. 09/262,126
Page 2

overpayment, to Deposit Account No. 07-1048 (Docket No. GC396-2). A duplicate of this paper is enclosed.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Richard T. Ito", written over a horizontal line.

Richard T. Ito
Registration No. 32,242

Date: March 20, 2001

Genencor International, Inc.
925 Page Mill Road
Palo Alto, CA 94304-1013
Tel: (650) 846-4020
Fax: (650) 845-6504

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**



Application No.: 09/262,126

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: The specification must be amended to include SEQ ID NOS. where applicable.

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

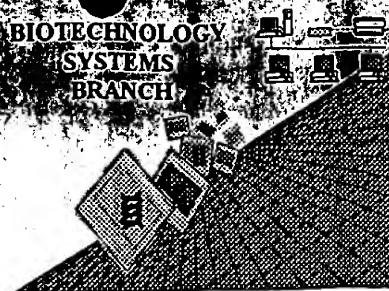
For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/262,126B
Source: 1600 RUSH
Date Processed by STIC: 2/22/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/262,126B

DATE: 02/23/2001
TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt
Output Set: N:\CRF3\02222001\1262126B.raw

3 <110> APPLICANT: Miller, Brian S.
4 Shetty, Jayarama K.
6 <120> TITLE OF INVENTION: Modified Forms of Pullulanase
9 <130> FILE REFERENCE: GC396-2
11 <140> CURRENT APPLICATION NUMBER: 09/262,126B
12 <141> CURRENT FILING DATE: 1999-03-03
14 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2794
20 <212> TYPE: DNA
21 <213> ORGANISM: B. deramificans
23 <221> NAME/KEY: misc_feature
24 <222> LOCATION: (1)...(2794)
25 <223> OTHER INFORMATION: n = A, T, C, or G
27 <400> SEQUENCE: 1
28 gatgggaaca cgacaacgat cattgtccac tahtttttgcc ctgctggtga ttatcaacct 60
29 tggagtctat ggatgtggcc aaaagacgga ggtggggctg aatacgattt caatcaacctg 120
30 gctgactctt ttggagctgt tgcaagtgtc gatattccag gaaacccaag tcaggtagga 180
31 attatcggtc gcaactcaaga ttggaccaaa gatgtgagcg ctgaccgcta catagattta 240
32 agcaaaggaa atgaggtgtg gcttgtagaa ggaacacgac aaatttttta taatgaaaaa 300
33 gatgctgagg atgcagctaa acccgctgta agcaacgctt atttagatgc ttcaaacag 360
34 gtgctgggta aacttagcca gccgttaact cttggggaag gnnnaagcgg ctttacggtt 420
35 catgacgaca cagcaataaa ggatattcca gtgacatctg tgaaggatgc aagtcttggt 480
36 caagatgtaa ccgctgtttt ggcaggtacc ttccaacata tttttggagg ttccgattgg 540
37 gcacctgata atcacagtac ttatttaaaa aaggtgacta acaactctca tcaattctca 600
38 ggagatcttc ctgaaggaaa ctaccaatat aaagtggctt taaatgatag ctggaataat 660
39 ccgagttacc catctgacaa cattaattta acagtcctcg ccggcgggtc acacgtcact 720
40 ttttcgtata ttccgtccac tcatgcaatc tatgacacaa ttaataatcc taatgcggat 780
41 ttacaagtag aaagcgggggt taaaacggat ctctgtagcg ttaactctagg ggaagatcca 840
42 gatgtgagcc atactctgtc cattcaaaaa gatggctatc aggcacagca ggtgatacct 900
43 cgtaatgtgc ttaattcatc acagtactac tattcaggag atgatcttgg gaatacctat 960
44 acacagaaaag caacaacctt taaagtctgg gcaccaactt ctactcaagg aaatgttctt 1020
45 ctttatgaca gtgcaacgg; ttctgtaaca aaaatcgta cttatgacggc atcggggccat 1080
46 ggtgtgtggg aagcaacggt taatcaaaaac cttgaaaatt ggtattacat gbatgaggta 1140
47 acaggccaag gctctaccog aacggctgtt gatecttatg caactgcgat tgcaccaaat 1200
48 ggaacgagag gcattgattgt ggacctggct aaaacagatc ctgctggctg gaacagtgat 1260
49 aaacatatta cgcacaagaa tatagaagat gaggtcatct atgaaatgga tgtccgtgac 1320
50 ttttccattg accctaattc gggatgaaa aataaaggga agtatttggc tcttacagaa 1380
51 aaaggaaaca agggccctga caacgtaaaag acggggatag attccttaaa acaacttggg 1440
52 attactcatg ttacgcttat gctgttttc gcatctaaca gtgctgatga aactgatcca 1500
53 acccaagata attgggggta tgacctcgc aactatgatg ttctggaagg gcagtatgct 1560
54 acaaatgcca atggtaatgc tegtataaaa gagtttaagg aaatggttct ttcaactccat 1620
55 cgtgaacaca ttgggggttaa catggatgtt gtctataatc atacctttgc caccgaaatc 1680
56 tctgacttcg ataaaattgt accagaatat tattaccgta cgatgatcca ggtaattata 1740
57 ccaacggatc aggtactgga aatgaaattg cangcngaaa ggccaatggt tcaaaaaattt 1800
58 attattgatt ccttaagta ttgggtcaat gagtatcata ttgacggctt ccgttttgac 1860

pp 1-2, 5
Does Not Comply
Corrected Diskette Needed

same error as
previous submit

→ <2207> ← insert the MANDATORY
numeric identifier

wherever

<2217, <2227,

or <2237 is
shown.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/262,126B

DATE: 02/22/2001

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

59 ttaatggcgc tgcctggaaa agacacgatg tccaaagctg cctcggagct tcatctatt 1920
 60 aatccaggaa ttgcaattta cggtagacca tggacgggtg gacccctctg actgcaagat 1980
 61 gacagcttc tgacaaaagg agctcaaaaa ggcattggag tagcgggtgt tattyacaat 2040
 62 ttacgaaaag cgttggacgg caatgtcttt gattcttcgg cccaagggtt cgcgacaggl 2100
 63 gcaacaggct taactgatgc aattaagaat ggcgttgagg ggagtattaa tgaactttac 2160
 64 tcttcacccg gtgagacaat taactatgtc acaagtcaty aaactacac tctttaggar 2220
 65 aaaaatagcc taagcaatcc taatgatcc gaaagcgatc ggaatcaat ggaatcaat 2280
 66 gcaacaggag ttgttatgac ctcaacaagg gtccattcca tgaaggcgg ggaatcaat 2340
 67 ctctgtanaa aaggcggcaa cgacaatagt tataatgcag gcgatgcgt caatgagttt 2400
 68 gattggagca ggaagctca atatccagat gttttcaact attatagagg gataatccac 2460
 69 ctctgtcttg atcaccagc ctcccgcaty aagacagcta atgaatcaa tagccacctc 2520
 70 caattccctaa atagtccaga gaacacagtg gcatatgaat taactgatca tgaataaaa 2580
 71 gacaaatggg gaaatatcat tgttgtttat aacccaaata aaactgtage aacccatcat 2640
 72 ttgccgagcg gaaatgggc aatcaatgct acgagcgcta aggtaggaga atccaccctt 2700
 73 ggtcaagcag agggaagtgt ccaagtacca ggtatatcta agatgatct tcatonagag 2760
 74 gtaagccacg accacggtaa aaagtaatag aaaa 2794

76 <210> SEQ ID NO: 2

77 <211> LENGTH: 958

78 <212> TYPE: PR1

79 <213> ORGANISM: B. deramificans

81 <220> FEATURE:

82 <221> NAME/KEY: VARIANT

83 <222> LOCATION: (1)...(956)

84 <223> OTHER INFORMATION: Xaa = Any Amino Acid

86 <220> FEATURE:

87 <221> NAME/KEY: VARIANT

88 <222> LOCATION: (957)...(957)

89 <223> OTHER INFORMATION: Xaa = gap of indeterminate length

91 <400> SEQUENCE: 2

92 Met Ala Lys Lys Leu Ile Tyr Val Cys Leu Ser Val Cys Leu Val Leu
 93 1 5 10 15
 94 Thr Trp Ala Phe Asn Val Lys Gly Gln Ser Ala His Ala Asp Gly Asn
 95 20 25 30
 96 Thr Thr Thr Ile Ile Val His Tyr Phe Cys Pro Ala Gly Asp Tyr Gln
 97 35 40 45
 98 Pro Trp Ser Leu Trp Met Trp Pro Lys Asp Gly Gly Gly Ala Glu Tyr
 99 50 55 60
 100 Asp Phe Asn Gln Pro Ala Asp Ser Phe Gly Ala Val Ala Ser Ala Asp
 101 65 70 75 80
 102 Ile Pro Gly Asn Pro Ser Gln Val Gly Ile Ile Val Arg Thr Gln Asp
 103 85 90 95
 104 Trp Thr Lys Asp Val Ser Ala Asp Arg Tyr Ile Asp Leu Ser Lys Gly
 105 100 105 110
 106 Asn Glu Val Trp Leu Val Glu Gly Asn Ser Gln Ile Phe Tyr Asn Glu
 107 115 120 125
 108 Lys Asp Ala Glu Asp Ala Ala Lys Pro Ala Val Ser Asn Ala Tyr Leu
 109 130 135 140
 110 Asp Ala Ser Asn Gln Val Leu Val Lys Leu Ser Gln Pro Leu Thr Leu
 111 145 150 155 160

Xaa can only represent
a single amino acid.

Per 1.822(d)(5)(e) of
new sequence rules,

"A sequence with a
gap or gaps shall
be presented as a
plurality of
separate sequences.

However, since only
one amino acid
follows gap, and
at least four
amino acids are
needed for a sequence
delete last amino
acid and adjust
the numbering to 9.

see p. 5

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

```

W--> 112 Gly Glu Gly Xaa Ser Gly Phe Thr Val His Asp Asp Thr Ala Asn Lys
      113              165              170              175
      114 Asp Ile Pro Val Thr Ser Val Lys Asp Ala Ser Leu Gly Gln Asp Val
      115              180              185              190
      116 Thr Ala Val Leu Ala Gly Thr Phe Gln His Ile Phe Gly Gly Ser Asp
      117              195              200              205
      118 Trp Ala Phe Asp Asn His Ser Thr Leu Leu Lys Lys Val Thr Asn Asn
      119              210              215              220
      120 Leu Tyr Gln Phe Ser Gly Asp Leu Pro Glu Gly Asn Tyr Gln Tyr Lys
      121 225              230              235              240
      122 Val Ala Leu Asn Asp Ser Trp Asn Asn Ser Tyr Pro Ser Asp Asn Ile
      123              245              250              255
      124 Asn Leu Thr Val Pro Ala Gly Gly Ala His Val Thr Phe Ser Tyr Ile
      125              260              265              270
      126 Pro Ser Thr His Ala Val Tyr Asp Thr Ile Asn Asn Pro Asn Ala Asp
      127              275              280              285
      128 Leu Gln Val Glu Ser Gly Val Lys Thr Asp Leu Val Thr Val Thr Leu
      129 290              295              300
      130 Gly Glu Asp Pro Asp Val Ser His Thr Leu Ser Ile Gln Thr Asp Gly
      131 305              310              315              320
      132 Tyr Gln Ala Lys Gln Val Ile Pro Arg Asn Val Leu Asn Ser Ser Gln
      133              325              330              335
      134 Tyr Tyr Tyr Ser Gly Asp Asp Leu Gly Asn Thr Tyr Thr Gln Lys Ala
      135              340              345              350
      136 Thr Thr Phe Lys Val Trp Ala Pro Thr Ser Thr Gln Val Asn Val Leu
      137              355              360              365
      138 Leu Tyr Asp Ser Ala Thr Gly Ser Val Thr Lys Ile Val Pro Met Thr
      139 370              375              380
      140 Ala Ser Gly His Gly Val Trp Glu Ala Thr Val Asn Gln Asn Leu Glu
      141 385              390              395              400
      142 Asn Trp Tyr Tyr Met Tyr Glu Val Thr Gly Gln Gly Ser Thr Arg Thr
      143              405              410              415
      144 Ala Val Asp Pro Tyr Ala Thr Ala Ile Ala Pro Asn Gly Thr Arg Gly
      145              420              425              430
      146 Met Ile Val Asp Leu Ala Lys Thr Asp Pro Ala Gly Trp Asn Ser Asp
      147              435              440              445
      148 Lys His Ile Thr Pro Lys Asn Ile Glu Asp Glu Val Ile Tyr Glu Met
      149 450              455              460
      150 Asp Val Arg Asp Phe Ser Ile Asp Pro Asn Ser Gly Met Lys Asn Lys
      151 465              470              475              480
      152 Gly Lys Tyr Leu Ala Leu Thr Glu Lys Gly Thr Lys Gly Pro Asp Asn
      153              485              490              495
      154 Val Lys Thr Gly Ile Asp Ser Leu Lys Gln Leu Gly Ile Thr His Val
      155              500              505              510
      156 Gln Leu Met Pro Val Phe Ala Ser Asn Ser Val Asp Glu Thr Asp Pro
      157              515              520              525
      158 Thr Gln Asp Asn Trp Gly Tyr Asp Pro Arg Asn Tyr Asp Val Pro Glu
      159 530              535              540
      160 Gly Gln Tyr Ala Thr Asn Ala Asn Gly Asn Ala Arg Ile Lys Glu Phe

```


RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

```

161 545          550          555          560
162 Lys Glu Met Val Leu Ser Leu His Arg Glu His Ile Gly Val Asn Met
163          565          570          575
164 Asp Val Val Tyr Asn His Thr Phe Ala Thr Gln Ile Ser Asp Phe Asp
165          580          585          590
166 Lys Ile Val Pro Glu Tyr Tyr Tyr Arg Thr Met Ile Gln Val Ile Ile
167          595          600          605
W--> 168 Pro Thr Asp Gln Val Leu Glu Met Lys Leu Xaa Ala Glu Arg Pro Met
169          610          615          620
170 Val Gln Lys Phe Ile Ile Asp Ser Leu Lys Tyr Trp Val Asn Glu Tyr
171 625          630          635          640
172 His Ile Asp Gly Phe Arg Phe Asp Leu Met Ala Leu Leu Gly Lys Asp
173          645          650          655
174 Thr Met Ser Lys Ala Ala Ser Glu Leu His Ala Ile Asn Pro Gly Ile
175          660          665          670
176 Ala Leu Tyr Gly Glu Pro Trp Thr Gly Gly Thr Ser Ala Leu Pro Asp
177          675          680          685
178 Asp Gln Leu Leu Thr Lys Gly Ala Gln Lys Gly Met Gly Val Ala Val
179 690          695          700
180 Phe Asn Asp Asn Leu Arg Asn Ala Leu Asp Gly Asn Val Phe Asp Ser
181 705          710          715          720
182 Ser Ala Gln Gly Phe Ala Thr Gly Ala Thr Gly Leu Thr Asp Ala Ile
183          725          730          735
184 Lys Asn Gly Val Glu Gly Ser Ile Asn Asp Phe Thr Ser Ser Pro Gly
185          740          745          750
186 Glu Thr Ile Asn Tyr Val Thr Ser His Asp Asn Tyr Thr Leu Trp Asp
187          755          760          765
188 Lys Ile Ala Leu Ser Asn Pro Asn Asp Ser Glu Ala Asp Arg Ile Lys
189 770          775          780
190 Met Asp Glu Leu Ala Gln Ala Val Val Met Thr Ser Gln Gly Val Pro
191 785          790          795          800
W--> 192 Phe Met Gln Gly Gly Glu Glu Met Leu Arg Xaa Lys Gly Gly Asn Asp
193          805          810          815
194 Asn Ser Tyr Asn Ala Gly Asp Ala Val Asn Glu Phe Asp Trp Ser Arg
195          820          825          830
196 Lys Ala Gln Tyr Pro Asp Val Phe Asn Tyr Tyr Ser Gly Leu Ile His
197          835          840          845
198 Leu Arg Leu Asp His Pro Ala Phe Arg Met Thr Thr Ala Asn Glu Ile
199 850          855          860
200 Asn Ser His Leu Gln Phe Leu Asn Ser Pro Glu Asn Thr Val Ala Tyr
201 865          870          875          880
202 Glu Leu Thr Asp His Val Asn Lys Asp Lys Trp Gly Asn Ile Ile Val
203          885          890          895
204 Val Tyr Asn Pro Asn Lys Thr Val Ala Thr Ile Asn Leu Pro Ser Gly
205          900          905          910
206 Lys Trp Ala Ile Asn Ala Thr Ser Gly Lys Val Gly Glu Ser Thr Leu
207          915          920          925
208 Gly Gln Ala Glu Gly Ser Val Gln Val Pro Gly Ile Ser Met Met Ile
209 930          935          940

```

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:01

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

W--> 210 Leu His Gln Glu Val Ser Pro Asp His Gly Lys Lys Xaa **Lys** *Delete*
 211 945 950 955
 213 <210> SEQ ID NO: 3
 214 <211> LENGTH: 718
 215 <212> TYPE: PRT
 216 <213> ORGANISM: B. subtilis
 218 <100> SEQUENCE: 3
 219 Met Val Ser Ile Arg Arg Ser Phe Glu Ala Tyr Val Asp Asp Met Asn
 220 1 5 10 15
 221 Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
 222 20 25 30
 223 Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
 224 35 40 45
 225 Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
 226 50 55 60
 227 His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
 228 65 70 75 80
 229 His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
 230 85 90 95
 231 Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
 232 100 105 110
 233 Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
 234 115 120 125
 235 Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
 236 130 135 140
 237 Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
 238 145 150 155 160
 239 Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
 240 165 170 175
 241 Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
 242 180 185 190
 243 Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
 244 195 200 205
 245 Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
 246 210 215 220
 247 Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
 248 225 230 235 240
 249 Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Ser Gly
 250 245 250 255
 251 Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
 252 260 265 270
 253 Val Asn Asp Phe Ala Gly Val Asp Glu Glu Lys Pro Leu Asp Ala Tyr
 254 275 280 285
 255 Asn Trp Gly Tyr Asn Pro Leu His Phe Phe Ala Pro Glu Gly Ser Tyr
 256 290 295 300
 257 Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
 258 305 310 315 320
 259 Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
 260 325 330 335

VERIFICATION SUMMARY

DATE: 02/22/2001

PATENT APPLICATION: US/09/262,126B

TIME: 12:09:02

Input Set : A:\GC396-2 seq.txt

Output Set: N:\CRF3\02222001\I262126B.raw

L:34 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:34 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
M:240 Repeated in SeqNo=1
L:67 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2